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March 17, 2004, 18:47:23 ; Search time 25:9237 Seconds (without alignments) 6683.183 Million cell updates/sec
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1 MAGKAABERGLPKGATPQDT......FMVLYYVSLRFIKQKPSQDW 673
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 8, Appli	Sequence 7, Appli	Sequence 4, Appli	Sequence 9, Appli	Sequence 175941,	Sequence 3, Appli	Seguence 6, Appli	Sequence 6, Appli	Sequence 1, Appli	Sequence 2, Appli	Sequence 14, Appl	Sequence 176182,	Sequence 245, App	Sequence 35, Appl	Sequence 61, Appl
SOMMERTES	ΩI	US-09-989-981A-8	US-10-090-455-7	US-09-989-981A-4	US-10-415-378-9	US-10-424-599-175941	US-09-837-992-3	US-09-989-981A-6	US-10-090-455-6	US-09-837-992-1	US-09-989-981A-2	US-09-866-866A-14	US-10-424-599-176182	US-10-108-605-245	US-09-981-353-35	US-10-120-687-61
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DB 10; Length 673; 0; Indels 0;

Query Match 100.0%; Score 3506; Best Local Similarity 100.0%; Pred. No. 0; Matches 673; Conservative 0; Mismatches

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Sequence 2, Appli Sequence 13, Appli Sequence 10, Appl Sequence 5, Appl Sequence 27, Appl Sequence 27, Appl Sequence 4, Appl Sequence 410, Appl Sequence 242078, Sequence 3135, Ap Sequence 3135, Ap Sequence 3135, Ap Sequence 54421, Ap Sequence 54421, Ap Sequence 54421, Ap Sequence 54421, Ap Sequence 54421, Ap Sequence 1442, Appl Sequence 14, Appl		System Methods of Use
US-10-405-806-2 US-09-961-086-1 US-09-866-866A-10 US-10-096-455-5 US-09-866-86A-27 US-09-866-86A-27 US-09-866-86A-27 US-09-866-86A-27 US-09-866-86A-27 US-10-090-455-4 US-10-090-455-4 US-10-090-455-4 US-10-424-599-42078 US-10-369-439-3799 US-10-369-439-3740 US-10-369-439-5740	ALIGNWE	The University of Texas & ABCG8: Compositions and OUS (09/989, 981A 7-23 60/252, 235 60/253, 645 8
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655 655 655 655 655 655 655 655 655 655	644 6444 10444 610 70 70 70 70 70 70 70 70 70 70 70 70 70	NT: Barnes, Robert NT: Tian, Hui NT: Trian, Hui NT: Tularik Inc. NT: Board of Regents, T) TI TULARINON ABCGS and Al FERENCE: 018781-007320US APPLICATION NUMBER: US 60. ILING DATE: 2002-07-2; PPLICATION NUMBER: US 60. ILING DATE: 2000-11-28 PPLICATION NUMBER: US 60. ILING DATE: 2000-11-28 E. Patentin Ver: 2.1 S. 8EQ ID NOS: 13 E. Patentin Ver: 2.1 S. 8M: Homo sapiens E. SM: Homo sapiens E. INFORMATION: human ABCG8 981A-8
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61 QVPWFEQLAQFKMPWTSPSCQNSCELGIQNLSFKVRSGQMLAIIGSSGCGRASLLDVITG
                                                 RGHGGKIKSGQIWINGQPSSPQLVRKCVAHVRQHNQLLPNLTVRETLAFIAQMRLPRTFS
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FEATURE:
CTHER INFORMATION: mouse ABCG8
US-09-989-9814-4
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Publication No. US20030027259A1
GENERAL INFORMATION:
APPLICANT: Chen, Hongyun
APPLICANT: Chen, Hongyun
TITLE OF INVENTION: NOVEL ABCG4 TRANSPORTER AND USES THEREOF
TITLE OF INVENTION: NOVEL ABCG4 TRANSPORTER AND USES THEREOF
CURRENT APPLICATION NUMBER: US/10/090,455
CURRENT FILING DATE: 2002-03-01
NUMBER OF SEQ ID NOS: 17
SEQ ID NO 7.
SEQ ID NO 7.
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ORGANISM: Homo sapiens
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                                                                                                                                                      RGHGGKIKSGQIWINGOPSSPQLVRKCVAHVRQHNQLLPNLTVRETLAFIAQWBLPRTFS
                                    1 MAGKAARERGLPKGATPQDTSGLQDRLFSSESDNSLYFTYSGQPNTLEVRDLNYQVDLAS
                                                        1 MAEKITKEETQLWNGTVLQDASGLQDSLESSESDNSLYFTYSGQSNTLEVRDLTYQVDIAS
                                                                                                                                                                                                                                  SGLDSFTAHNLVTTLSRLAKGNRLVLISLHQPRSDIFRLFDLVLLMTSGTPIYLGAAQQM
                                                                                                61 OVPWFEQLAQFKMPWTSPSCONSCELGIQNLSFKVRSGOMLALIGSSGCGRASLLDVITG
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             Gaps
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Sequence 9, Application US/10415378
Fublication No. US20040014945A1
GENERAL INFORMATION:
APPLICANT: INCYTE CORPORATION; TANG, Y. Tom
APPLICANT: VUE, Henry; NGUYEN, Danniel B.;
APPLICANT: YAO, Monique G.; BAUGHN, Mariah R.;
APPLICANT: AAO, Monique G.; BAUGHN, Mariah R.;
APPLICANT: SANJANWALA, Madhusudan M.; RAMKUMAR, Jayalaxmi;
APPLICANT: SANJANWALA, Madhusudan M.; RAMKUMAR, Jayalaxmi;
APPLICANT: ARVIZU, Chandra S.; GIETZEN, Kimberly J.;
APPLICANT: LAL, Preeti G.; AZIMZAL; Yalda;
APPLICANT: THORNION, Michael B.; Lu, Dyung Aina M.;
APPLICANT: TRIBOULEY, Catherine M.; WARREN, Bridget A.;
APPLICANT: RAUMANN, Brigette E.; POLICKY, Jennifer L.;
APPLICANT: KEARNEY, Liam
TITLE OF INVENTION: TRANSPORTERS AND ION CHANNELS
81.9%; Pred. No. 1.7e-281;
ive 52; Mismatches 69; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               660 SLKLIKOKSIODW 672
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Best Local Similarity 81.9
Matches 551, Conservative
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Sequence 175941, Application US/10424599
Publication No. US20040031072A1
APPLICANT: LA Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
PILE REFERENCE: 38-21(53223)
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; OTHER INFORMATION: Incyte ID No. US20040014945A1 6585710CD1
US-10-415-378-9
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FILE REFERENCE: F.1.0270 US. NO. 415,378
CURRENT FILING DATE: 2003-05-07
PRIOR APPLICATION NUMBER: PCT/USO1/46055
PRIOR APPLICATION NUMBER: US 60/250,790
PRIOR FILING DATE: 2000-12-01
PRIOR FILING DATE: 2000-12-01
PRIOR FILING DATE: 2000-11-07
PRIOR FILING DATE: 2000-11-09
PRIOR FILING DATE: 2000-11-09
PRIOR FILING DATE: 2000-11-09
PRIOR FILING DATE: 2000-11-09
PRIOR FILING DATE: 2000-11-03
PRIOR APPLICATION NUMBER: US 60/245,904
PROR FILING DATE: 2000-11-03
PRIOR PILING DATE: 2000-11-27
NUMBER OF SEQ ID NOS: 40
SGEQ ID NO 9
LENGTH: 374
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ORGANISM: Homo sapiens
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US-10-424-599-175941
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us-09-989-981a-8.rapb

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FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                393 VWWKQFXLLLKRAWMQASRDAPTNKVRARMSIASAIIFGSVFWRMGNSQTSIQQBRMGLLQ 452
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                                                                                                                                                                                                                                                                                                  61 AEAPTSGKVTPVTIGWRNINCSLSDKSSKSARFLLKNVSGBAKPGRLLAIMGPSGSGKTT 120
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                                                                                                                                                                                                                                                                                60 SQVPWFEQLAQFKMPWTSPSC-----QNSCELGIQNLSFKVRSGQMLAIIGSSGCGRAS
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Batent No. US20020081687A1

GENERAL INFORMATION:
APPLICANT: Tian, Hui
APPLICANT: Schultz, Joshua
APPLICANT: Schultz, Joshua
APPLICANT: Shan, Bei
APPLICANT: Tulatik Inc.
TITLE OF INVENTION: Sitosterolemia Susceptibility Gene (SSG):
TITLE OF INVENTION: And Methods of Use
FILE REPERENCE: 018781-006020US
CURRENT APPLICATION NUMBER: US/09/837,992
                                                                                                                                                                                                                          Query Match
21.4%; Score 751; DB 12; Length 7:
Best Local Similarity 30.9%; Pred. No. 4.1e-66;
Matches 178; Conservative 115; Mismatches 229; Indels
                                                                                                                                                                              ; OTHER INFORMATION: Clone ID: PAT_MRT3847_129893C.1.pep
US-10-424-599-175941
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CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 175941
LENGTH: 725
LENGTH: 725
CREATURE: PRT
ORGANISM: Glycine max
FEATURE: Unsure
LOCATION: (1)...(725)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE: CREATURE: CREATURE: (1)...(725)
FEATURE: CREATURE: (2)...(725)
FEATURE: CREATURE: (3)...(725)
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US-09-837-992-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 476 AMLYYELBDGLYTTGPYFFAKILGELPEHCAYIIIYGMPTYWLANLRPGLQPFLLHFLLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          255 LSRLAKGNRLVLISLHQPRSDIFRLFDLVLLMTSGTPIYLGAAQHMVQYFTAIGYPCPRY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   135 NGQPSSPQLVRKCVAHVRQHNQLLPNLTVRETLAFIAQMRLPRTFSQAQRDKRVEDVIAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       422 AEACLMSWTIGFLYFG-----HGSIQLSFWDTAALLFMIGALIPFNVILDVISKCYSER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   578 INLSSLWTVPAWISKVSFLRWCFEGLMKIQFSRRTYKMPLGNLTIAVS 625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: human sitosterolemia susceptibility gene; OTHER INFORMATION: amino acid sequence
US-09-837-992-3
                                                                                                                                                                                                                                                                                                                         Length 651
                                                                                                                                                                                                                                                                                                                       Ouery Match
19.9%; Score 697; DB 9; Length 65
Best Local Similarity 28.9%; Pred. No. 9.8e-61;
Matches 187; Conservative 124; Mismatches 241; Indels
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CURRENT FILING DATE: 2001-04-18
PRIOR APPLICATION NUMBER: US 60/198,465
PRIOR FILING DATE: 2000-04.18
PRIOR FILING DATE: 2000-04.18
PRIOR FILING DATE: 2000-05-15
NUMBER OF SEQ ID NOS: 45
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3
LENGTH: 651
TYPE: PRT
ONGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         476 AMLYYELEDGLYTTGPYFFAKILGELPEHCAYIIIYGMPTYWLANLRPGLQPFLLHFLLV 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76 TSPSCQNSCELGIQNLSFKVRSGQMLAIIGSSGCGRASILDVITGR-GHGGKIKSGQIWI 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       255 ISRLAKGNRLVLISLHQPRSDIFRLFDLVLLMTSGTPIYLGAAQHMVQYFTAIGYPCPRY 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   363 AETKOLDEDICVESSVIPLDINCLPSPIK-MPGAVQOFITLIRRQISNDFRDLPTLLIHG 421
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                                                                                                                                                                                                                                                                                                                                                                                                                                64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               536 WLVVFCCRIMALAAALLPTFHMASFFS-----GFM
                                                                                                                                                                                                                                                                                                                                                                                                  16 TPODISGLODRLFSSESONSLYFTYSGOPNILEVRDLNYQVDLASGVPWFEQLAQFKMPW
                                                                                                                                                                                                                                                                                                                                                                                                                      195 LRLRQCADTRVGNMYVRGLSGGERRRVSIGVQLLWNPGILILDEPTSGLDSFTAHNLVKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   422 AEACLMSWTIGFLYFG-----HGSIQLSFWDTAALLFMIGALIPFNVILDVISKCYSER
                                                                                                                                                                                                                                                                                                                                                                     Gaps
APPLICANT: Tian, Hui
APPLICANT: Tularik Inc.
APPLICANT: Tularik Inc.
APPLICANT: Tularik Inc.
Tularik Inc.
Tularik Lor
Tularik OF INVENTION ABGGS and ABGG8: Compositions and Methods of Use
FILE REFERENCE: 018791-007320US
CURRENT APPLICATION NUMBER: US 60/252,235
PRIOR APPLICATION NUMBER: US 60/252,235
PRIOR FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
LENGTH: 651
                                                                                                                                                                                                                                                                                                                                                                     96;
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Best Local Similarity 28.9%; Pred. No. 9.8e-61;
Matches 187; Conservative 124; Mismatches 241; Indels
                                                                                                                                                                                                                                                                         FEATURE:
, OTHER INFORMATION: human ABCG5 (hABCG5)
US-09-989-981A-6
                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
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135 NGQPSSPQLVRKCVAHVRQHNQLLPNLTVRETLAFIAQMRLPRTFSQAQRDKRVEDVIAE

LSRLAKGNRLVLISLHQPRSDIFRLFDLVLLMTSGTPIYLGAAQHMVQYFTAIGYPCPRY 314

LVELARRNRIVVLTIHQPRSELFQLFDKIAILSFGELIFCGTPAEMLDFFNDCGYPCPEH

235 315

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SNPADFYVDLTSIDRRSREQELATREKAQSLAALF------LEKVRDLDDFLWK 362

SNPFDPYMDLTSVDTQSKEREIETSKRVQMIESAYKKSAICHKTLKNIERMKHL-----

76 TSPSCONSCELGIQNLSFXVRSGOMLAIIGSSGCGRASLLDVITGR-GHGGKIKSGQIWI 134

TPODTSGLODRLFSSESDNSLYFTYSGOPNTLEVRDLNYQVDLASQVPWFEQLAQFYMPW

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TRQI-----LKDVSLYVESGQIMCILGSSGSGKTTLLDAMSGRLGRAGTF-LGEVVV

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116

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64

Gaps

96;

Length 651;

Query Match
Best Local Similarity 28.9%; Pred. No. 9.8e-61;
Matches 187; Conservative 124; Mismatches 241; Indels

; TYPE: PRT; ORGANISM: Homo sapiens US-10-090-455-6

AND USES THEREOF

; Publication No. US20030027259A1
; GENERAL INFORMATION:
APPLICANT: Chen, Hongyun
; APPLICANT: Le Bihan, Stephane
; TITLE OF INVENTION: NOVEL ABCG4 TRANSPORTER AND
FILE REPRENCE: 100103.406
; CURRENT APPLICATION NUMBER: US/10/090,455
; CURRENT FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 6

194 174 348

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ABACLMSMTIGFLYFG-----HGSIQLSFMDTAALLFMIGALIPFNVILDVISKCYSER

447 AVSDQESQDGLYQKWQMMLAYALHVLPFSVVATMIFSSVCYWTLGLHPEVARF----- 499

AMLYYELEDGLYTTGPYFFAKILGELPEHCAYIIIYGMPTYWLANLRPGLQPFLLHFLLV

-----GYFSAALLAPHLIGEFLTLVILGIVONPNIVNSVVALLSIAGVLVGSGFL

536 WLVVFCCRIMALAAALLPTFHMASFFS-

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-NALYNSFYLAG----GFM 577

363 AETKOLDEDICVESSVTPLDINCLPSPTK-MPGAVQOFTTLIRRQISNDFRDLPTLLIHG 421

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578 INLSSLWTVPAWISKVSFLRWCFEGLMKIOFSRRTYKMPLGNLTIAVS 625
                       RESULT 9
US-09-837-992-1
; Sequence 1, Application US/09837992
; Patent No. US20020081687A1
; GENERAL INFORMATION:
; APPLICANT: Tan, Hui
; APPLICANT: Schultz, Joshua
; APPLICANT: Schultz, Joshua
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SULT 8 -10-090-455-6 Sequence 6, Application US/10090455

d 셤 g ď g Ś 유 8 a à ò ò à à à 360 KDPPGWFGKLGVLLRRVTRNLMRNKQAVIMRLVQNLIMGLFLIFYLLRVQNNTLKGAVQD 419 420 RVGLLYQLVGATPYTGMLNAVNLFPMLRAVSDQESQDGLYHKWQMLLAYVLHVLPFSVIA 479 566 480 TVIFSSVCYWTLGLYPEVARF-------GYFSAALLAPHLIGEFLTLVLL 522 ------YNSFYLAGGFMINLSSLWTVPAWISKVSFLRWCFEGLMKIQFS 609 581 VRETLRYTAMLALCRS-SADPYNKKVBAVMTELSLSHVADQMIGSYNFGGISSGERRNS 203 VLLMTSGTPIYLGAAQHMVQYFTAIGYPCPRYSNPADFYVDLTSIDRRSREQELATREKA 342 QSLAALF------LEKVRDLDDFLWKAETKDLDEDTCVESSVTPLDTNCLPSPT 390 K-MPGAVQQFTTLIRRQISNDFRDLPTLLIHGAEACLMSMTIGF--LYFGHGSIQLSFMD 447 448 TAALLFMIGALIPFNVILDVISKCYSERAMLYYELEDGLYTTGPYFFAKILGELPEHCAY 507 45 NTLEVRDLNYQVDLASQV-PWFEQLAQFKMPWTSPSCQNSCELGI-QNLSFKVRSGQMLA 102 103 IIGSSGCGRASLLDVITGRGHGGKIKSGQIWINGQPSSPQLVRKCVAHVRQHNQLLPNLT 162 VRETLAFIAQMRLPRIFSQAQRDKRVEDVIAELRLRQCADIRVGNMYVRGLSGGERRRVS 222 IGVQLLWNPGILILDEPTSGLDSFTAHNLVKTLSRLAKGNRLVLISLHQPRSDIFRLFDL 282 Compositions 8 523 GIVQNPNIVNSIVALLSISGLLIGSGFIRNIQEMPIPLKILGYFTFQKYCCEILVVNEF-610 RRTYKMPLGNLTIAVSGDKILSAMELDSYPLYAI----------YLIVI HSLGVLHVSYSV--SNRVGPW------WNIKSCQQKWDRQILKDVSLYIESGQIMC 508 IIIYGMPTYWLANLRPGLQPFLLHFLLVWLVVFCCRIMALAAAALLPTFHWASFFSNAL-Gaps OTHER INFORMATION: mouse sitosterolemia susceptibility gene (SSG) : OTHER INFORMATION: amino acid sequence US-09-837-992-1 APPLICANT: Tularik Inc.

TITLE OF INVENTION: Sitosterolemia Susceptibility Gene (SSG): Computing OF INVENTION: and Methods of Use
TITLE OF INVENTION: and Methods of Use
FILE REPERENCE: 018781-00602003
CURRENT APPLICATION NUMBER: US/05/837,992
CURRENT FILING DATE: 2001-04-18
PRIOR FILING DATE: 2000-04-18
PRIOR FILING DATE: 2000-04-18
PRIOR FILING DATE: 2000-05-15
NUMBER OF SEQ ID NOS: 45
SEQ ID NO 1
LENGTH: 652 Query Match
19.6%; Score 688.5; DB 9; Length 652;
Best Local Similarity 28.1%; Pred. No. 7.1e-60;
Matches 188; Conservative 125; Mismatches 233; Indels 123; TYPE: PRT ORGANISM: Mus musculus 37 163 145 223 283 264 343 391 8 8 8 8 8 8 임 ద à ద ò ద 8 6 6 6 g ò ò

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37 HSLGVLHVSYSV--SNRVGPW-------WNIKSCQQKWDRQILKDVSLYIESGQINC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      103 IIGSSGCGRASLLDVITGRGHGGKIKSGQIWINGQPSSPQLVRKCVAHVRQHNQLLPNLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45 NTLEVRDLNYQVDLASQV-PWFEQLAQFKMPWTSPSCQNSCELGI-QNLSFKVRSGQMLA
                                                                                                  GENERAL INCOMENTATION:

APPLICANT: Hobbs, Helen H.

APPLICANT: Shan, Bei

APPLICANT: Barnes, Robert

APPLICANT: Tian, Hui

APPLICANT: Tian, Hui

APPLICANT: Tularik Inc.

APPLICANT: WINSTICAN: ABGGB and ABGGB: Compositions and Methods of Use FILE REFERENCE: 018781-007320US

CURRENT APPLICATION NUMBER: US 60/252,235

PRIOR FILING DATE: 2000-11-20

PRIOR FILING DATE: 2000-11-28

NUMBER OF SEQ ID NOS: 13

SOFTWARE: PATENTING PATE: 2000-11-28

NUMBER OF SEQ ID NOS: 13

SEQ ID NOS: 13

LENGTH: 652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 652;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 19.6%; Score 688.5; DB 10; Best Local Similarity 28.1%; Pred. No. 7.1e-60; Matches 188; Conservative 125; Mismatches 233;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ) OTHER INFORMATION: mouse AECG5 (mAECG5)
US-09-989-981A-2
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RESULT 10
US-09-989-981A-2
; Sequence 2, Application US/09989981A
; Publication No. US20030049730A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Mus musculus
PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            163
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Sequence 176182, Application US/10424599

Sequence US20040031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: Zhou Yihua

APPLICANT: Cao Yongwei

ITILE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REPERENCE: 38-21(53223)B

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT APPLICATION NUMBER: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 175182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          236 SIHQPSSEVFALFDDLFLLSGGETXYFGEAKSAIEFFAEAGFPCPRKRNPSDHFLRCINS 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 296 DFDIVTATIKGSQRIHDVPNSADPFMNLATAE----IKATLVEKYR---RSTYARRAKNR 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   349 IQELSTBEGLQP-----PTQHGSQASWWKQLSTLTKRSFVNMCRDVGYYWLRIIIYI 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Y'GVAA'ILANFLSSFPFLVALALTISTITYNMVKFRPGISHFVFFFLNIYSCISVIESL 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --DLTSIDRRSREQ-------ELATREKAQSLAALFLEKVRDLDDFLWKAETKDL 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          369 DEDICVESSVIPLDINCLPSPIKMPGAV---QOFITLIRRQISNDFRDLPTLLIHGAEAC 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   486 LYTTGPYFFAKILGELPEHCAYIIIYGMPTYWLANLRPGLQPFLLHFLLVWLVVFCCRIM 545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                208 MYVRGLSGGERRRVSIGVQLLWNPGILILDEPTSGLDSFTAHNLVKTLSRLAKGNRLVLI 267
                                                                        561 IGPWLSWLQYPSIPRYGFTALQYNEFLGGEF-CPGFNVTDNSTCVNSYAICTGNEYLINQ 619
501 KTVDAFFIMMFTLIMVAYTASSMALAIATGQSVVSVATLLMTIAFVFMMLFSGLLVNLRT 560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              583 LWTVPAWISKVSFLRWCFEGLMKIQPSRRTYKMPLGNLT-----IAVSGDKIL--S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88 IONLSFKVRSGOMLAIIGSSGCGRASILDVITGRGHGGKIKSGOIWINGQPSSPQLVRKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VAHVROHNOLLPNLTVRETLAFIAOMRLPRTFSQAQRDKRVEDVIAELRLRQCADTRVGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STHOPRSDIFRLFDLVLLMTSGTPIYLGAAQHMVQYFTAIGYPCPRYSNPADFYV----
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| NAME/KEX: unsure
| LOCATION: (1).. (695)
| OTHER INFORMATION: unsure at all Xaa locations
| PEATURE:
| PEATURE:
| OTHER INFORMATION: clone ID: PAT_MRT3847_130109C.1.pep
                                                                                                                                                 Query Match
18.7%; Score 657; DB 12;
Best Local Similarity 27.9%; Pred. No. 1.2e-56;
Matches 173; Conservative 129; Mismatches 253;
                                                                                                                       632 AMELDSYPLYAIYLIVIGLSGGFMVLYYVSLRFIKQ 667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                             US-10-424-599-176182
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Sequence 14, Application US/0986666A

Patent No. US20201022441

GENERAL INFORMATION:

APPLICANT: Sortentino, Brian

APPLICANT: Schuetz, John

TITLE OF INNEWIND: A Method of Identifying and/or Isolating Stem Cells

TILE OF INNEWIND: A Method of Identifying and/or Isolating Stem Cells

FILE REFERENCE: 1340-1-021CIP2

CURRENT APPLICATION NUMBER: US/09/866,866A

CURRENT FILING DATE: 2001-08-30

PRIOR FILING DATE: 1990-05-31

PRIOR FILING DATE: 1990-05-27

PRIOR FILING DATE: 1990-05-27

PRIOR FILING DATE: 1990-05-28

NUMBER OF SEQ ID NOS: 27

SOFTWARE: PatentIn Version 3.0

SEQ ID NO 14
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                           ----YLIVI 648
                                                 582 ---YGL---NFTCGGSNTSML-----NHPMCAITGGVQFIEKTCPGATSRFTANFLLLY 629
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19.0%; Score 666; DB 9; Le
Best'Local Similarity 28.0%; Pred. No. 1.3e-57;
Matches 178; Conservative 127; Mismatches 255;
                           RRIYKMPLGNLTIAVSGDKILSAMELDSYPLYAI
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                                                                                                                                  630 GFIPALVIL 638
                                                                                                           649 GLSGGFMVL 657
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US-09-866-866A-14
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                                           ASFFSNALYNSFYLAGGFMINLSSLWTVPAWISKVSFLRWCFEGLMKIQFS---RRTYKM 615
78
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                                                                                                              616 PLGNLTIAVSGDKILSAMELDSYPLYAIYLIVIGLSGGFMVLYYVSLR 663
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NAME/KEY: misc feature

No. US20020160382A1 5517972CD1
US-09-981-353-35
                                                                                                                                       TSSNTTCPSSGKVILETLNFSAADLFLDYVGLAILIVSFRVLAYLALR
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Best Local Similarity 27.2%; Pred. No. 3.1e-55;
Matches 187; Conservative 139; Mismatches 273;
                                                                                                                                                                                                                                                                                                                      CANCER
                                                                                                                                                                                                                        Sequence 35, Application US/09981353
Patent No. US20020160382A1
GENERAL INFORMATION:
APPLICANT: Lasek, Amy W.
ITILE OF INVENTION: GENES EXPRESSED IN COLON CAN
FILE REPERENCE: PA-0038 US
CURRENT APPLICATION UNDER: US/09/981,353
CURRENT PILING DATE: 2001-10-11
NUMBER OF SEQ ID NOS: 194
SEQ ID NO 35
LENGTH: 655
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
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US-09-981-353-35
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                                                                                                                                                                                                                                                              Sequence 245, Application US/10108605

Publication No. US20020160934A1

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Bachmann, Jane

APPLICANT: Bachmann, Jane

APPLICANT: Bachmann, Jane

APPLICANT: Wandar Kim

TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FROM DROSOPHILA MELANOGASTER THAT ENCODE

TITLE OF INVENTION: PAPPLICATION NUMBER: US/10/108,605

CURRENT APPLICATION NUMBER: US/10/108,605

CURRENT APPLICATION NUMBER: US/10/1142

PRIOR PILING DATE: 2000-01-14

PRIOR PILING DATE: 2000-01-14

NUMBER OF SEQ ID NOS: 361

SOFTHARE: PATENTIN VEY: 2.1

SOFTHARE: PATENTIN VEY: 2.1

SOFTHARE: PATENTIN VEY: 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        269 VILTIHQPSSELFELFDKILLMAEGRVAFLGTPSEAVDFFSYVGAQCPTNYNPADFYVQV 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    329 LAV---VPGREIBSRDRIAKICDNFAISKVARDMEQLL---ATKNLEK-------PLE 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TNCLPSP----TKMPGAVQQFTTLIRRQISNDFRDLPTLLIHGAEACLMSMTIGFLYFGH 438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             439 GSIQLSFMDTAALLFMIGALIPFNVILDVISKCYSERAMLYYELEDGLYTTGPYFFAKIL 498
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88 IQNLSFKVRSGQMLAIIGSSGCGRASILDVITGRGHGG--KIKSGQIWINGQPSSPQLVR 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KCVAHVROHNOLLPNLTVRETLAFIAOMRLPRIFSQAQRDKRVEDVIABLRLRQCADTRV 205
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                                                    578
                                                                                                      SYKONDLIGLERD-----PLLPGDPKLTGEYVITHMIGIELNHSKWWDLAALFVILI--- 629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         G-NMYVRGLSGGERRRVSIGVQLLWNPGILILDEPTSGLDSFTAHNLVKTLSRLAKGNRL 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VLISLHOPRSDIFRLFDLVLLMTSGTPIYLGAAQHMVQYFTAIGYPCPRYSNPADFYVDL 324
                                                                                    651
                                     S20 MWVVASLVPNFLMGIITGAGIIGIMMTSGFFRLLSDL-PKPVMRYPISYISYGSWAIQG
                                                                                      -----IMKIOFSRRTYKMPLGNLTIAVSGDKILSAM---ELDS---YPLYAIYLIVIGLS
                  546 ALAAAALLPTFHMASFFSNALYNSFYLAGGFMINLSSLWTVPAW---ISKVSFLRWCFEG
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18.7%; Score 656; DB 13; 1
Best Local Similarity 30.3%; Pred. No. 1.4e-56;
Matches 178; Conservative 113; Mismatches 265;

// TYPE: PRT
// ORGANISM: Drosophila melanogaster
US-10-108-605-245

                                                                                                                                                       652 GGFMVLYYVSLRFIKOKPS 670
                                                                                                                                                                                - CYRLLFFTVLKF-KERAS 646
                                                                                                                                                                                                                                            RESULT 13
US-10-108-605-245
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507 FVMMFTLMMVAYSASSMALALAAGGSVVSVATLLMTICFVFNMIFSGLLVNLTTIASWLS 566
                                 120 HGAEACLMSMTIGFLYFGHGSIQLSFMDTAALLFMIGALIPFNVILDVISKCYS----- 473
                                                                                                                                                                                                                                                          589 WISKVSFLRWCFEGLMKIQFSRRTYKMPLGNLT-----IAVSGDKIL--SAMELDSYP 639
                                                                                                                                                                                                                                                                                           567 WLOYFSIPRYGFIALOHNEFLGONF-CPGLNATGNNPCNYATCTGEEYLVKQGIDLSPWG 625
349 LHQLSGGEKKKKITVFKEISYTTSFC------HQLRWVSKRSFKNLLGNPQASIA 397
                                                                                                                                   398 QIIVTVVLGLVİĞAİYFĞLKNDSTGIQNRAGVLFFL------TTNQCFSSVSAVE
                                                                                                         ----ERAMLYYELEDGLYTTGPYFFAKILGE-LPEHCAYIIIYGMPTYWLANLRPGLQPF
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Job time : 27.9237 secs
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Publication No. US20030082155A1

GENERAL INFORMATION:

TITLE OF INVENTION: Mellitus

FILE REPRENCE: 3284/1235B

CURRENT APPLICATION NUMBER: US/10/120,687

CURRENT FILING DATE: 1999-12-06

PRIOR FILING DATE: 1999-12-06

PRIOR FILING DATE: 2001-09-25

PRIOR FILING DATE: 2000-06-28

PRIOR FILING DATE: 2000-10-06

PRIOR FILING DATE: 2000-11-06

NUMBER OF SEQ ID NOS: 61

SOFTWARE: 2001-12-06

NUMBER OF SEQ ID NOS: 61

SED ID NO 61

LENGTH: 655
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                       529 LLHFLLVWLVVFCCRIMALAAAALLPTFHMASFFSNALYNSFYLAGGFMINLSSLWTVPA 588
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89; Gaps
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18.3%; Score 642.5; DB 14; Length
Best Local Similarity 27.2%; Pred. No. 3.1e-55;
Matches 187; Conservative 139; Mismatches 273; Indels
                                                                                               WISKVSFLRWCFEGLMKIOFSRRTYKMPLGNLT
                                                                                                                                                                    640 LYAIYLIVIGLSGGFMVLYYVSLRFIKQ 667
                                                                                                                                                                                           ) ORGANISM: Homo sapiens
US-10-120-687-61
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